

DOT POINT

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IB BIOLOGY AHL



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Introduction

What the book includes

This book provides questions and answers for each dot point in the IB Biology Additional Higher Level (AHL) syllabus from the International Baccalaureate Diploma Programme for Biology:

- Nucleic Acids and Proteins
- Cell Respiration and Photosynthesis
- Plant Science
- Genetics
- Human Health and Physiology

Format of the book

The book has been formatted in the following way:

1.1 Subtopic from syllabus.

1.1.1 Assessment statement from syllabus.

1.1.1.1 First question for this assessment statement.

1.1.1.2 Second question for this assessment statement.

The number of lines provided for each answer gives an indication of how many marks the question might be worth in an examination. As a rough rule, every two lines of answer might be worth 1 mark.

How to use the book

Completing all questions will provide you with a summary of all the work you need to know from the syllabus. You may have done work in addition to this with your teacher as extension work. Obviously this is not covered, but you may need to know this additional work for your school exams.

When working through the questions, write the answers you have to look up in a different colour to those you know without having to research the work. This will provide you with a quick reference for work needing further revision.



Command Terms and Verbs to Watch

account, account for State reasons for, report on, give an account of, narrate a series of events or transactions.

analyse Interpret data to reach conclusions.

annotate Add brief notes to a diagram or graph.

apply Use an idea, equation, principle, theory or law in a new situation.

assess Make a judgement of value, quality, outcomes, results or size.

calculate Find a numerical answer showing the relevant stages in the working (unless instructed not to do so).

clarify Make clear or plain.

classify Arrange into classes, groups or categories.

comment Give a judgement based on a given statement or result of a calculation.

compare Give an account of similarities and differences between two (or more) items, referring to both (all) of them throughout.

construct Represent or develop in graphical form.

contrast Show how things are different or opposite.

deduce Reach a conclusion from the information given.

define Give the precise meaning of a word, phrase or physical quantity.

demonstrate Show by example.

derive Manipulate a mathematical relationship(s) to give a new equation or relationship.

describe Give a detailed account.

design Produce a plan, simulation or model.

determine Find the only possible answer.

discuss Give an account including, where possible, a range of arguments for and against the relative importance of various factors, or comparisons of alternative hypotheses.

distinguish Give differences between two or more different items.

draw Represent by means of pencil lines.

estimate Find an approximate value for an unknown quantity.

evaluate Assess the implications and limitations.

examine Inquire into.

explain Give a detailed account of causes, reasons or mechanisms.

extract Choose relevant and/or appropriate details.

extrapolate Infer from what is known.

identify Find an answer from a given number of possibilities.

justify Support an argument or conclusion.

label Add labels to a diagram.

list Give a sequence of names or other brief answers with no explanation.

measure Find a value for a quantity.

outline Give a brief account or summary.

predict Give an expected result.

propose Put forward a point of view, idea, argument, suggestion etc for consideration or action.

recall Present remembered ideas, facts or experiences.

show Give the steps in a calculation or derivation.

sketch Represent by means of a graph showing a line and labelled but unscaled axes but with important features (for example, intercept) clearly indicated.

solve Obtain an answer using algebraic and/or numerical methods.

state Give a specific name, value or other brief answer without explanation or calculation.

suggest Propose a hypothesis or other possible answer.

summarise Express concisely the relevant details.

synthesise Put together various elements to make a whole.

Nucleic Acids and Proteins

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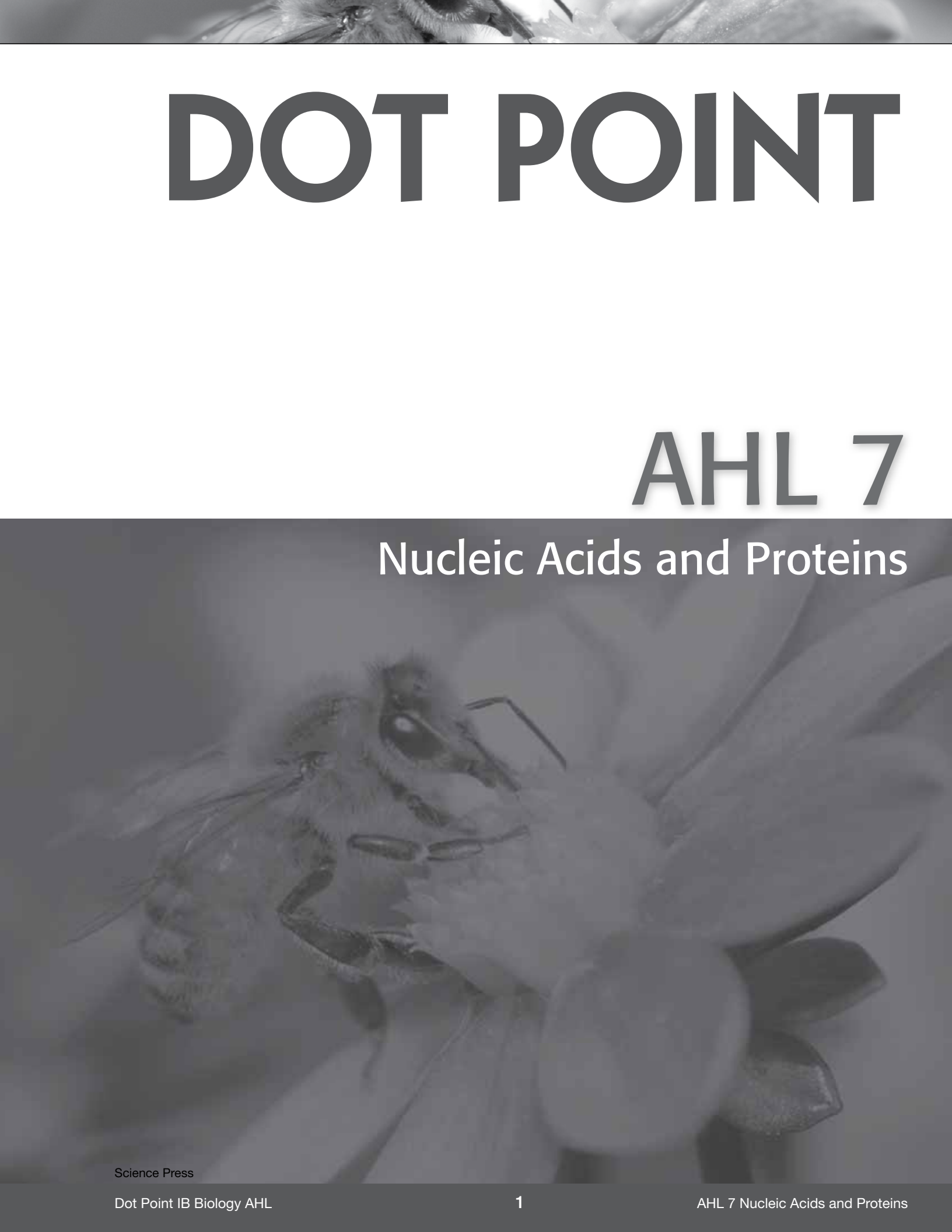
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A close-up photograph of a bee on a flower, serving as a background for the page. The bee is positioned in the lower half, facing left, with its head and thorax visible. The flower's petals are in the foreground, slightly out of focus.

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AHL 7

Nucleic Acids and Proteins

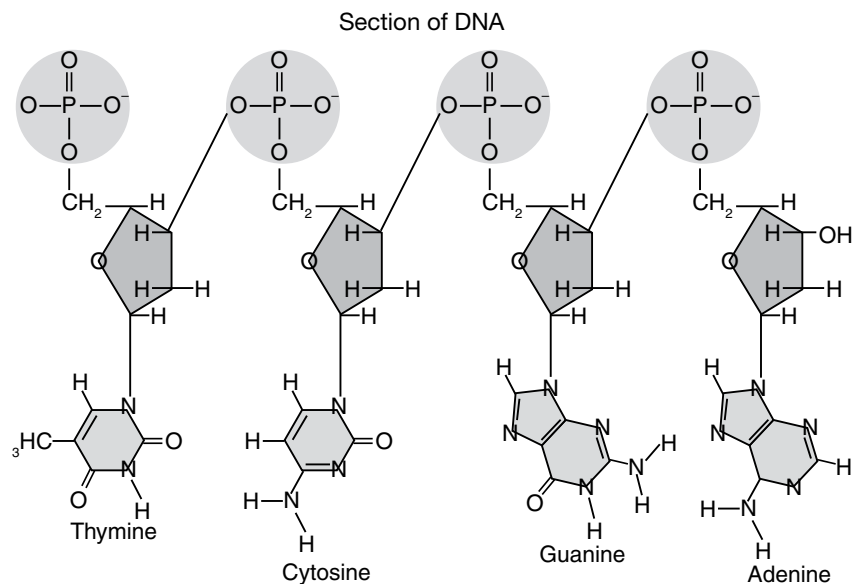
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7.1

DNA structure. © IBO 2007

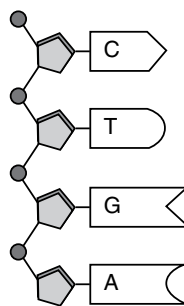
7.1.1 Describe the structure of DNA, including the antiparallel strands, 3'-5' linkages and hydrogen bonding between purines and pyrimidines. © IBO 2007

7.1.1.1 A section of DNA has directionality. On the diagram, mark in the carbon numbers to show the 5' to 3' directionality of this polynucleotide section.



7.1.1.2 Complete the diagram by drawing the complementary DNA strand and labelling the 5' and 3' ends to show what is meant by antiparallel strands of DNA.

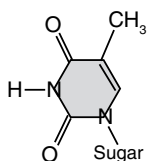
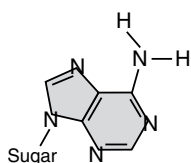
Antiparallel strands of DNA



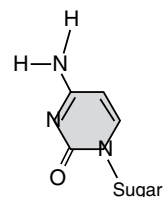
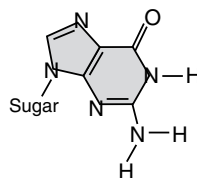
7.1.1.3 Annotate the diagram to show the bonding between purines and pyrimidines.

Bonding between purines and pyrimidines

Adenine-thymine bonding



Guanine-cytosine bonding





7.1.2 Outline the structure of nucleosomes. © IBO 2007

7.1.2.1 What is a nucleosome?

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7.1.2.2 What is histone?

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7.1.2.3 Outline why nucleosomes are referred to as ‘beads’.

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7.1.2.4 Draw a diagram of a nucleosome.

7.1.2.5 Histones from different eukaryotes are very similar to each other. What does this suggest about the evolutionary importance of histones?

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7.1.3 State that nucleosomes help to supercoil chromosomes and help to regulate transcription. © IBO 2007

7.1.3.1 Identify the function of nucleosomes in supercoiling.

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7.1.3.2 Identify the function of nucleosomes in regulating transcription.

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7.1.4 Distinguish between unique or single-copy genes and highly repetitive sequences in nuclear DNA. © IBO 2007

7.1.4.1 What is meant by highly repetitive sequences?

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7.1.4.2 What is meant by unique or single-copy genes?

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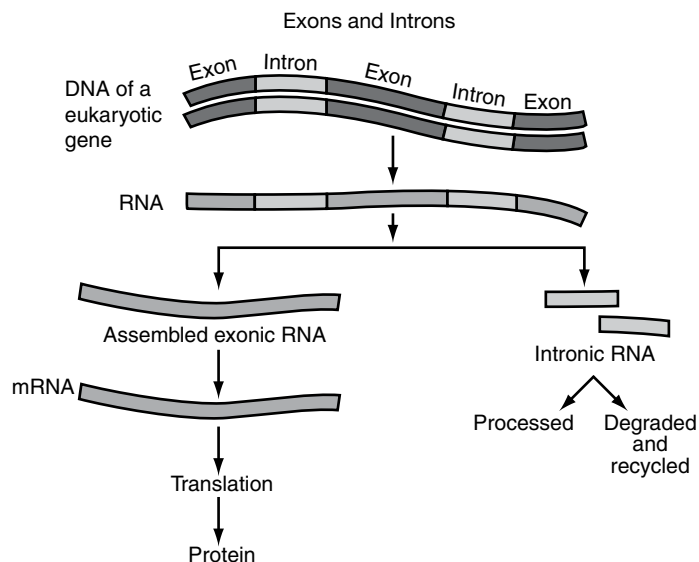
7.1.4.3 Use the data to construct a column graph to show the different types of DNA sequences in the human genome.

Type of DNA sequence	Percentage of human genome (%)
Repetitive DNA including transposable elements	44
Introns and regulatory sequences	24
Unique non-coding DNA	15
Repetitive DNA not transposable elements	15
Exons	1.5

7.1.5 State that eukaryotic genes can contain exons and introns. © IBO 2007

7.1.5.1 Distinguish between exons and introns.

7.1.5.2 The diagram shows exons and introns in a section of eukaryotic DNA.
Explain what is happening in the diagram.



7.1.5.3 Outline how alternative splicing of introns within a gene can introduce variability in a protein.

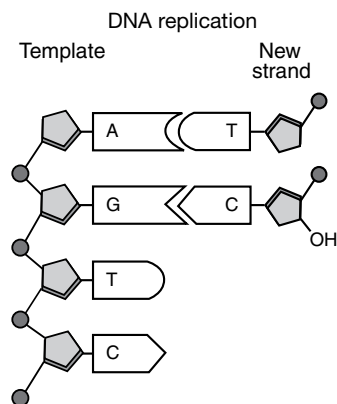
7.1.5.4 What are spliceosomal introns?

7.2 DNA replication. © IBO 2007

7.2.1 State that DNA replication occurs in a 5' → 3' direction. © IBO 2007

7.2.1.1 Outline the directionality of DNA elongation during replication.

7.2.1.2 Label the 5' and 3' ends of the template strand and new strand. To the new strand add a nucleotide to show how replication occurs in a 5' → 3' direction.



7.2.2 Explain the process of DNA replication in prokaryotes, including the role of enzymes (helicase, DNA polymerase, RNA primase and DNA ligase), Okazaki fragments and deoxynucleoside triphosphates. © IBO 2007

7.2.2.1 Identify the main difference between prokaryotic DNA and eukaryotic DNA.

7.2.2.2 Outline the main function of helicase.

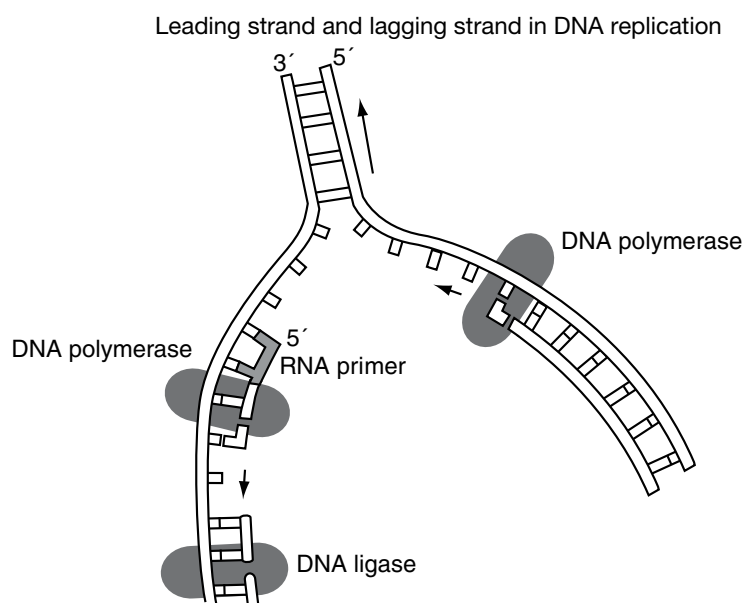
7.2.2.3 Describe the function of a primer and RNA primase.

7.2.2.4 What are Okazaki fragments?

7.2.2.5 Outline the main function of DNA polymerase and distinguish between DNA polymerase I (pol I) and DNA polymerase III (pol III).

7.2.2.6 Outline the function of DNA ligase.

7.2.2.7 Annotate the diagram to explain DNA replication with the synthesis of the leading strand and the lagging strand.



7.2.2.8 Outline the function of deoxynucleoside triphosphates.

7.2.3 State that DNA replication is initiated at many points in eukaryotic chromosomes. © IBO 2007

7.2.3.1 Suggest why it is important for DNA replication to begin at many points along a eukaryotic chromosome.

7.3 Transcription. © IBO 2007

7.3.1 State that transcription is carried out in a 5' → 3' direction. © IBO 2007

7.3.1.1 Identify the direction of transcription.

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7.3.2 Distinguish between the sense and antisense strands of DNA. © IBO 2007

7.3.2.1 Define the sense strand of DNA.

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7.3.2.2 Define the antisense strand of DNA.

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7.3.2.3 Compare the sense strand of DNA and the antisense strand of DNA with the associated section of mRNA.

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7.3.2.4 Compare the sense strand of DNA and the antisense strand of DNA with the associated section of tRNA.

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7.3.2.5 The mRNA codes – CCU, CCC, CCA and CCG all code for the amino acid proline. Construct a table to show the sense strand, antisense strand, mRNA and tRNA codes for these four codes for proline.

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7.3.3 Explain the process of transcription in prokaryotes, including the role of the promoter region, RNA polymerase, nucleoside triphosphates and the terminator. © IBO 2007

7.3.3.1 What is a promoter region?

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7.3.3.2 Define RNA polymerase.

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7.3.3.3 Compare RNA polymerase with DNA polymerase.

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7.3.3.4 Describe the different forms of nucleoside triphosphates.

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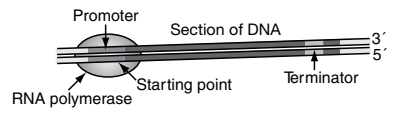
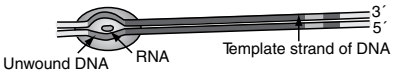
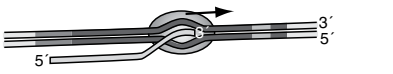
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7.3.3.5 What is a terminator?

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7.3.3.6 Complete the table to summarise the stages of transcription.

Diagram	Description of stage of transcription
	
	
	
	

7.3.4 State that eukaryotic RNA needs the removal of introns to form mature mRNA. © IBO 2007

7.3.4.1 In eukaryotes the transcript RNA is often called pre-mRNA. Briefly outline what happens to pre-mRNA to form mature mRNA.

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7.4 Translation. © IBO 2007

7.4.1 Explain that each tRNA molecule is recognised by a tRNA-activating enzyme that binds a specific amino acid to the tRNA, using ATP for energy. © IBO 2007

7.4.1.1 What is tRNA?

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7.4.1.2 Draw a typical tRNA and indicate the location of the anticodon and where the amino acid is attached.

7.4.1.3 What are tRNA-activating enzymes?

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7.4.1.4 Outline the two steps involved in binding an amino acid to a tRNA.

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7.4.1.5 Describe the bonding of the amino acid to a tRNA.

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7.4.2 Outline the structure of ribosomes, including protein and RNA composition, large and small subunits, three tRNA binding sites and mRNA binding sites. © IBO 2007

7.4.2.1 Draw a diagram to show the two subunits of a ribosome.

7.4.2.2 What are ribosomes made of?

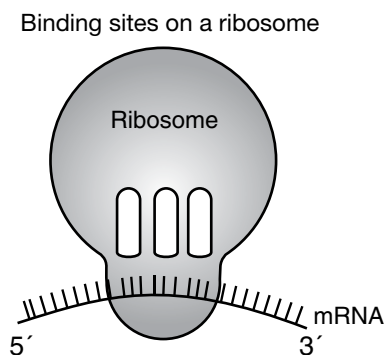
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7.4.2.3 Annotate the diagram to show the three tRNA binding sites and the mRNA binding sites.



7.4.2.4 Compare the ribosomes of bacteria, archaea and eukaryotes.

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7.4.3 State that translation consists of initiation, elongation, translocation and termination. © IBO 2007

7.4.3.1 Identify the main stages in translation.

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7.4.4 State that translation occurs in a 5' → 3' direction. © IBO 2007

7.4.4.1 Identify the direction of translation.

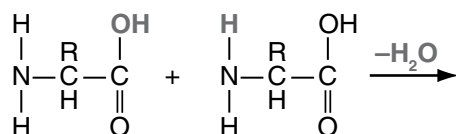
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7.4.4.2 At which end are you likely to find the start codon?

.....

7.4.5 Draw and label a diagram showing the structure of a peptide bond between two amino acids. © IBO 2007

7.4.5.1 The equation shows two amino acids combining. Complete the equation and highlight the peptide bond.



7.4.6 Explain the process of translation, including ribosomes, polysomes, start codons and stop codons. © IBO 2007

7.4.6.1 Define polysome.

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7.4.6.2 Name the start codon on mRNA and the corresponding anticodon on the first tRNA.

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7.4.6.3 Outline the role of a stop codon.

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.....

7.4.6.4 Complete the table to summarise the process of translation.

Stages of translation	
Diagram of stage	Description of stage

7.4.7 State that free ribosomes synthesise proteins for use primarily within the cell, and that bound ribosomes synthesise proteins primarily for secretion or for lysosomes. © IBO 2007

7.4.7.1 Identify a difference between free ribosomes and bound ribosomes.

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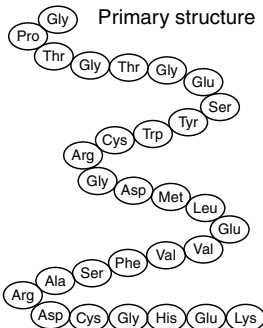
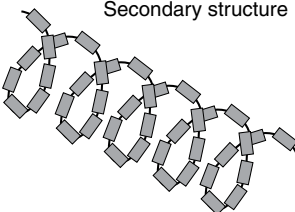
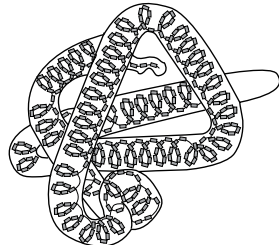
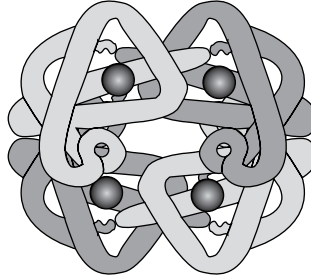
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7.5

Proteins. © IBO 2007

7.5.1 Explain the four levels of protein structure, indicating the significance of each level. © IBO 2007

7.5.1.1 Complete the table to summarise the four levels of protein structure.

Diagram of protein	Description	Significance
Primary structure 		
Secondary structure 		
Tertiary structure 		
Quaternary structure 		

7.5.2 Outline the difference between fibrous and globular proteins, with reference to two examples of each protein type. © IBO 2007

7.5.2.1 Complete the table to compare fibrous proteins and globular proteins.

Characteristic	Fibrous protein	Globular protein
Shape		
Polypeptide chains		
Properties		
Examples and function		

7.5.3 Explain the significance of polar and non-polar amino acids. © IBO 2007

7.5.3.1 Outline why some amino acids are polar while others are non-polar.

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7.5.3.2 Explain why the polar/non-polar property of an amino acid is important.

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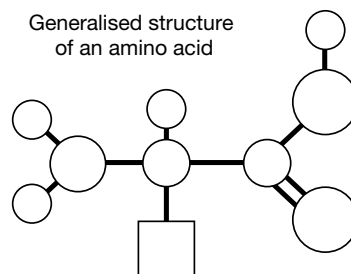
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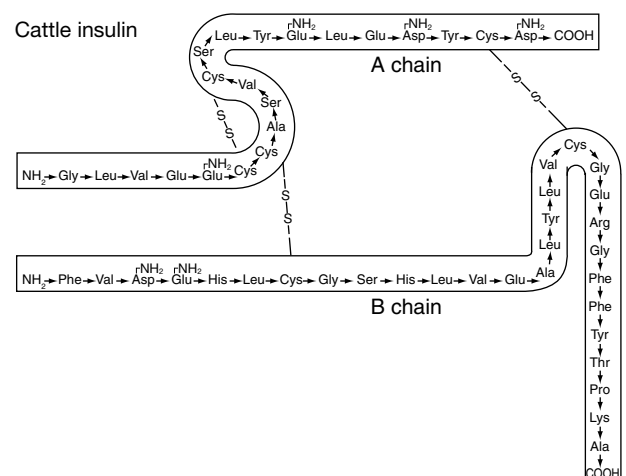
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7.5.3.3 The diagram shows the generalised structure of an amino acid. Identify each component.



7.5.3.4 The diagram shows the sequence of amino acids in cattle insulin. Insulin consists of two chains with two disulfide bonds holding the chains together. The third disulfide bond causes a loop within a single chain. Insulin is not synthesised in its active form; it needs to fold into its correct conformation to become active. Insulin is a globular protein with the interior containing mostly non-polar amino acid side chains and the exterior mostly polar side chains.

Discuss how the arrangement of non-polar and polar amino acids and disulfide bonds give insulin its shape.



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7.5.4 State four functions of proteins, giving a named example of each. © IBO 2007

7.5.4.1 Complete the table to summarise four functions of proteins.

Function	Description of function	Example
Enzyme		
Hormone		
Structure		
Transport		

7.6

Enzymes. © IBO 2007

7.6.1 State that metabolic pathways consist of chains and cycles of enzyme-catalysed reactions. © IBO 2007

7.6.1.1 What is a metabolic pathway?

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7.6.1.2 Outline how enzymes are involved in metabolic pathways.

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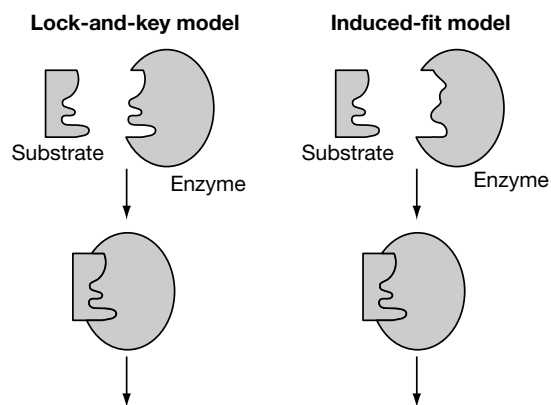
7.6.2 Describe the induced-fit model. © IBO 2007

7.6.2.1 What is the active site?

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7.6.2.2 Complete the diagram to show the difference between the lock-and-key model and the induced-fit model for a catabolic enzyme.



7.6.2.3 Explain how our understanding of how enzymes act on their substrates shows the development of scientific theory.

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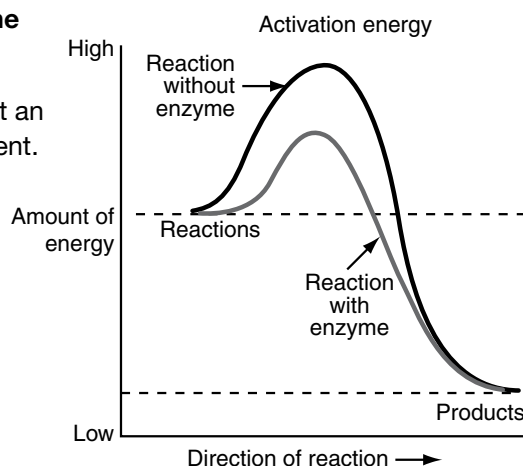
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7.6.3.1 Explain the graph showing an exothermic reaction without an enzyme and an exothermic reaction with an enzyme present.



7.6.4 Explain the difference between competitive and non-competitive inhibition with reference to one example of each. © IBO 2007

7.6.4.1 Define competitive inhibition.

7.6.4.2 Define non-competitive inhibition.

7.6.4.3 Complete the table to compare competitive and non-competitive inhibition for this substrate and enzyme.

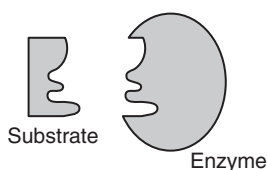


Diagram	Type of inhibition	How inhibition works	Example
 Substrate Enzyme			
 Substrate Enzyme			

7.6.5 Explain the control of metabolic pathways by end-product inhibition, including the role of allosteric sites. © IBQ 2007

7.6.5.1 Define an allosteric regulated enzyme.

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7.6.5.2 Define the allosteric site.

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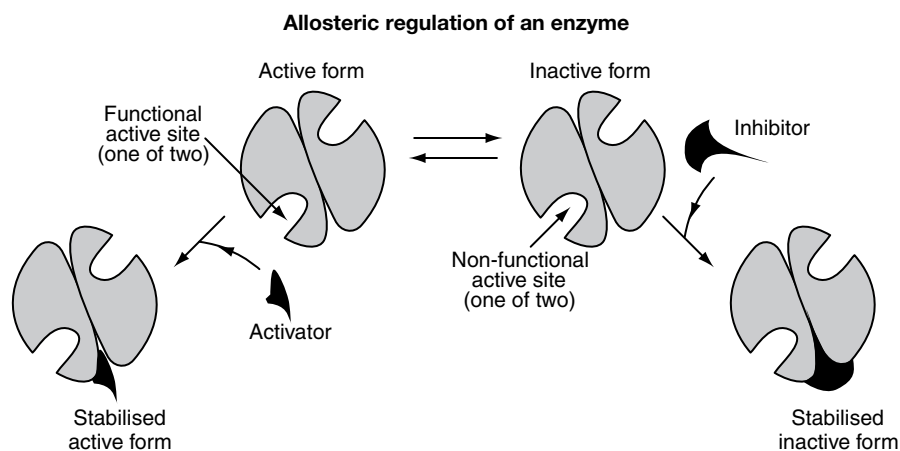
7.6.5.3 Compare allosteric activators and allosteric inhibitors.

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7.6.5.4 Refer to the diagram to explain how allosteric activators and allosteric inhibitors control the activities of an enzyme.



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7.6.5.5 What is cooperativity?

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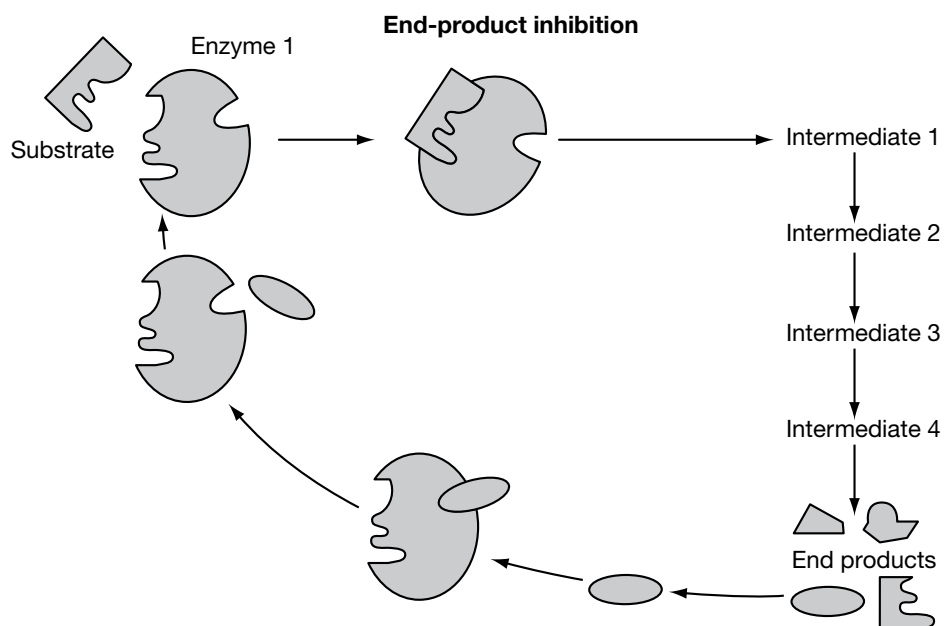
7.6.5.6 Define end-product inhibition.

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7.6.5.7 Annotate the flow chart to explain how end-product inhibition operates.



7.6.5.8 What is mixed inhibition?

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7.6.5.9 Suggest why many drugs resemble the substrate for specific reactions.

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DOT POINT

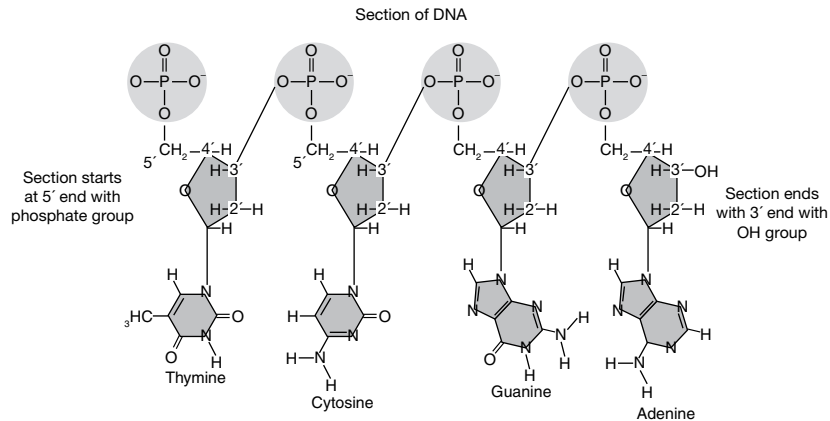
ANSWERS



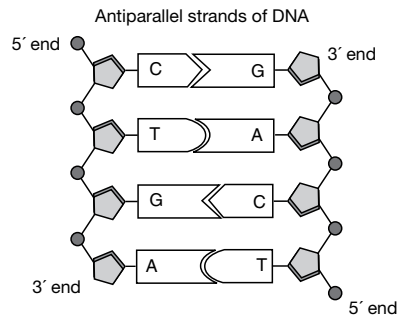
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AHL 7 Nucleic Acids and Proteins

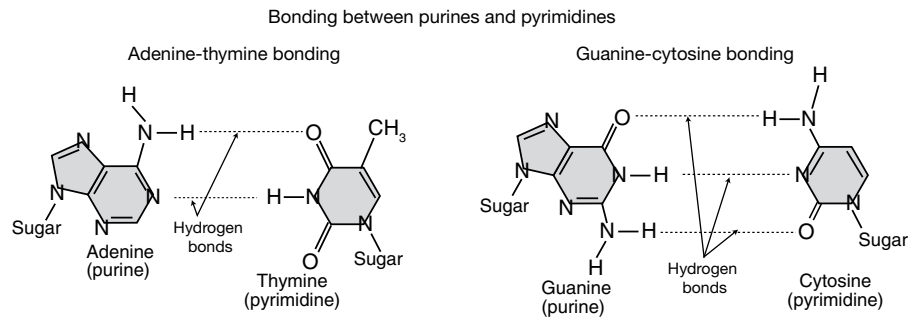
7.1.1.1



7.1.1.2



7.1.1.3



7.1.2.1

Nucleosome is the basic unit of eukaryotic DNA consisting of a section of DNA wound around a protein core which contains eight histone proteins (two copies of each of four types of histone). It is held together by another histone protein.

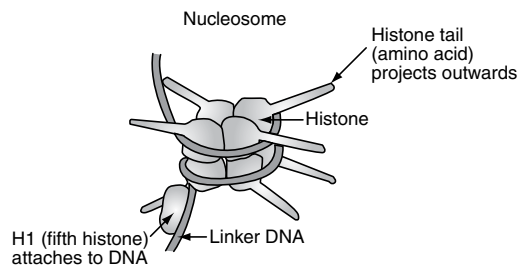
7.1.2.2

Histone is a small protein that has a high amount of positively charged amino acids (lysine and arginine) that bind to negatively charged DNA (phosphate groups). Histones are important in the structure and packaging of chromatin and in transcription.

7.1.2.3

Nucleosomes are often referred to as 'beads' because unfolded chromatin on electron micrographs looks like a series of beads on a string. The nucleosomes are the 'beads' and the 'string' is linker DNA.

7.1.2.4



7.1.2.5 Since histones from different eukaryotes are similar to each other, it suggests the histone gene has been conserved throughout evolutionary history as it is very important in organising DNA within cells.

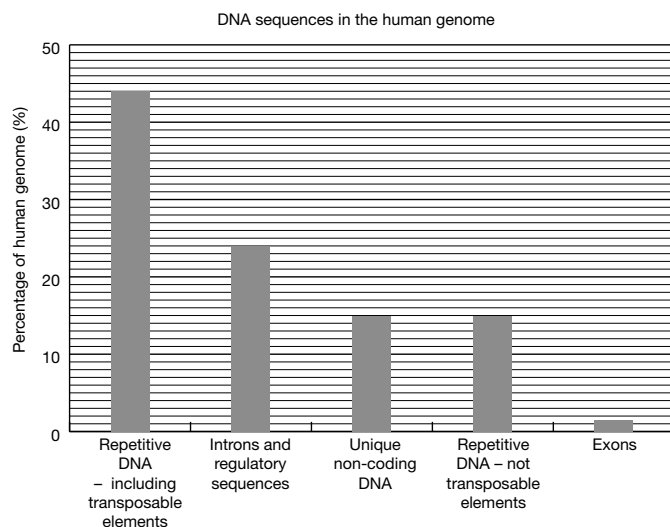
7.1.3.1 Interactions between histone tails, linker DNA and between adjacent nucleosomes leads to DNA supercoiling. Supercoiling reduces the space needed for DNA and is required for DNA/RNA synthesis.

7.1.3.2 Chromatin normally has a compact structure with nucleosomes interacting causing DNA supercoiling. Transcription cannot occur in such a region. If the histone tails are acetylated, the chromatin becomes less compact, there is a looser structure and transcription can begin. Thus nucleosomes regulate transcription and gene expression.

7.1.4.1 Highly repetitive sequences (satellite DNA) were once called 'junk DNA'. They are sections of DNA that exist in multiple copies in the genome (e.g. 10^5 times repeated). They make up between 5-45% of a genome and consist of 5-300 base pairs per repeat.

7.1.4.2 Unique or single-copy genes are sections of DNA that encodes protein or RNA. In humans these exons comprise around 1.5% of a genome.

7.1.4.3



7.1.5.1 Exons are coding sections of eukaryotic DNA, while introns are non-coding sections between the exons.

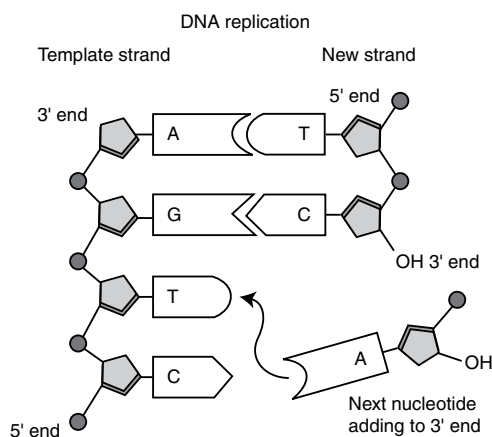
7.1.5.2 The diagram shows that eukaryotic DNA contains both exons and introns. During transcription, both exons and introns are transcribed to form a long primary RNA transcript. RNA processing removes the introns leaving the exonic RNA to form mRNA. Translation occurs and a protein is formed. The intronic RNA that has been removed is either degraded and recycled or processed, e.g. to form microRNAs.

7.1.5.3 In eukaryotes introns are spliced from the pre-mRNA. An alternative splicing of introns within a gene means that the code for the protein on mRNA will be slightly different to the usual code when usual splicing occurs. This variation in sequences means the protein will have slight variations which could slightly alter its properties.

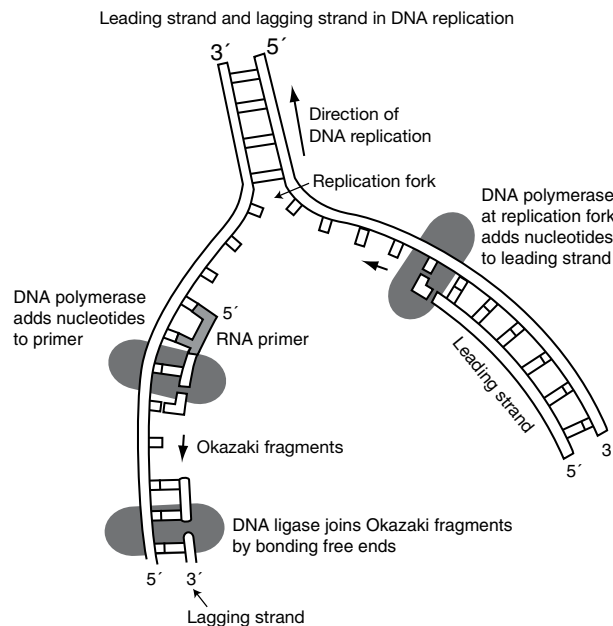
7.1.5.4 Spliceosomal introns or nuclear introns are only found in eukaryotes and are spliced by the spliceosome and a series of small nuclear RNAs.

7.2.1.1 During replication the next nucleotide to be added is joined to the 3' end under the influence of DNA polymerase. This means that replication only occurs in the 5' → 3' direction.

7.2.1.2



- 7.2.2.1** The main part of a prokaryotic genome is the double-stranded circular DNA that has a small amount of protein, while eukaryotes have linear DNA with large amounts of protein.
- 7.2.2.2** Helicases are enzymes that move directionally along two annealed nucleic acid strands, e.g. during DNA replication, helicase will break the hydrogen bonds between the two strands of DNA.
- 7.2.2.3** A primer is a short polynucleotide with a free 3' end. It is needed to start the replication process. Primase is activated by DNA helicase to synthesise short RNA primers. Primase can also act as a stopping mechanism to keep the leading strand from outpacing the lagging strand.
- 7.2.2.4** Okazaki fragments are segments of the lagging strand of a replicating section of DNA. They consist of the primer with added DNA nucleotides.
- 7.2.2.5** DNA polymerase is an enzyme that catalyses the polymerisation of deoxyribose-nucleotides into a DNA strand. During DNA replication the enzyme uses the original strand as a template to form the new strand always adding to the 3' end of the new strand. DNA pol III acts on the leading strand by continuously adding DNA nucleotides to the primer. On the lagging strand DNA pol III elongates an Okazaki fragment in bacteria by adding nucleotides to the primer. DNA pol I acts on the leading strand by removing the primer from the 5' end and replaces it with DNA, while on the lagging strand it removes the primer from the 5' end of each Okazaki fragment and replaces each with DNA.
- 7.2.2.6** DNA ligase joins the sugar-phosphate backbones of the Okazaki fragments together to complete the new single DNA strand.
- 7.2.2.7**



- 7.2.2.8** Deoxyribonucleoside triphosphates consist of an organic base, a deoxyribose sugar and three phosphate groups (dATP, dCTP, dGTP and dTTP). They form hydrogen bonds between their organic bases and the complementary base of the section of DNA that is acting as the template. As each nucleotide attaches to the new strand, the second and third phosphate groups are removed from the deoxyribose triphosphate changing it into a deoxyribosnucleotide (organic base, deoxyribose sugar and phosphate).
- 7.2.3.1** Replication is needed to begin at many points along a eukaryotic chromosome to speed the process and decrease the time needed for total chromosome replication.
- 7.3.1.1** Transcription occurs in the 5' → 3' direction.
- 7.3.2.1** The sense strand of DNA is the strand that is *not* transcribed into mRNA during polypeptide synthesis.
- 7.3.2.2** The antisense strand of DNA is the strand that is transcribed into mRNA during polypeptide synthesis.
- 7.3.2.3** The antisense strand of DNA is complementary to the mRNA. The sense strand has the same code sequence as the mRNA (except for uracil replacing thymine).
- 7.2.3.4** tRNA is complementary to mRNA. The sense strand of DNA is complementary to the tRNA. The antisense strand has the same code sequence as the tRNA (except for uracil replacing thymine).

7.3.2.5

DNA sense strand	DNA antisense strand (part of transcription)	mRNA	tRNA
CCT	GGA	CCU	GGA
CCC	GGG	CCC	GGG
CCA	GGT	CCA	GGU
CCG	GGC	CCG	GGC

7.3.3.1 A promoter region is a specific sequence of DNA codes that indicates the beginning of a section for transcription. RNA polymerase attaches to the promoter region to begin transcription.

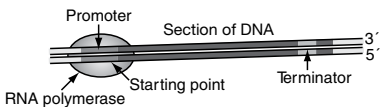
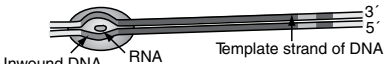
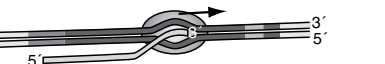
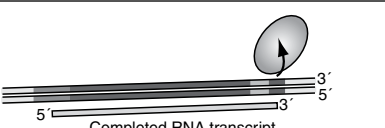
7.3.3.2 RNA polymerase is an enzyme that separates the two strands of DNA and joins ribonucleotides together to form RNA during transcription.

7.3.3.3 Both DNA polymerase and RNA polymerase can link nucleotides along a template to assemble a polynucleotide. DNA polymerase requires a primer to initiate the process, DNA polymerase does not need a primer to start a new chain.

7.3.3.4 Ribonucleoside triphosphates and deoxyribonucleosides are both nucleoside triphosphates. Differences between these two forms relate to the differences between ribose sugar and deoxyribose sugar. Ribose and deoxyribose are both pentose sugars but deoxyribose carries an -H instead of an -OH at position 2.

7.3.3.5 The terminator is a specific sequence of DNA codes found in prokaryotes that signals the end of a gene and the section to be transcribed. The terminator signals RNA polymerase to release the transcript RNA.

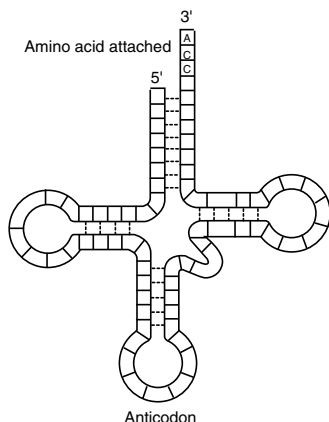
7.3.3.6

Diagram	Description of stage of transcription
	Initiation: RNA polymerase binds to the promoter region of the gene to be transcribed.
	First stage: RNA polymerase causes the two DNA strands to unwind and begins to hook ribonucleosides together to form mRNA
	Elongation: RNA moves along the antisense strand elongating the RNA transcript in the 5' → 3' direction. As it moves it unwinds the DNA strands and the region behind re-forms into a double helix.
	Termination: When RNA polymerase reaches terminator, transcription stops, the RNA transcript is released. The RNA polymerase detaches and moves away.

7.3.4.1 Pre-mRNA in eukaryotes is the complete transcript of the section of DNA transcribed. The coding section for the gene contains many introns that need to be removed. The pre-mRNA is edited in RNA processing. One end of the pre-mRNA is capped and the other end is tailed. A large part of the pre-mRNA is then removed to form mature mRNA.

7.4.1.1 tRNA is a type of RNA that takes amino acids from the cytoplasm and transfers them to a ribosome during translation. The amino acids are joined together to make a polypeptide following the genetic code on mRNA.

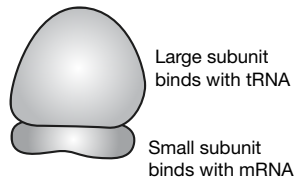
7.4.1.2 tRNA



- 7.4.1.3** There are 20 different tRNA-activating enzymes, as there are 20 different amino acids. Each enzyme joins a particular amino acid to a tRNA.
- 7.4.1.4** The two steps in binding an amino acid to a tRNA are: 1. The tRNA-activating enzyme binds ATP and the required amino acid to form an activated amino acid and ATP loses its energy. 2. The newly formed complex is bound to tRNA at the 3' end with the CCA sequence.
- 7.4.1.5** There is a condensation reaction between the CCA sequence and the amino acid to be joined to the tRNA. A covalent bond is formed when the –OH of the adenine (A) reacts with the –OH of the –COOH of the amino acid to form water. The covalent bond is broken during translation and the amino acid hooks on to the end of the polypeptide chain with a peptide bond.

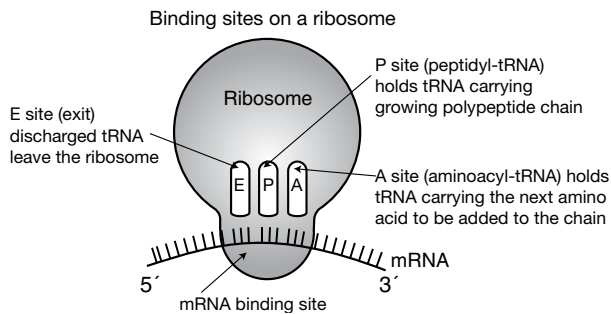
7.4.2.1

Ribosome structure

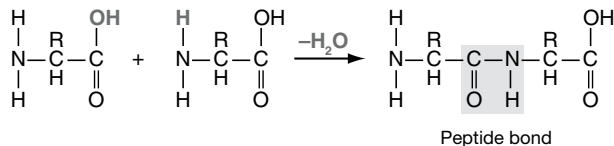


- 7.4.2.2** Both subunits of ribosomes consist of proteins and ribosomal RNA (rRNA). The smaller subunit consists of one molecule of rRNA and proteins while the larger subunit consists of two molecules of rRNA and proteins, including the enzyme peptidyl transferase.

7.4.2.3

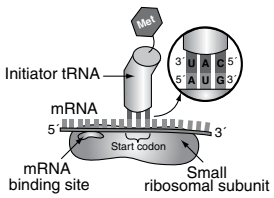
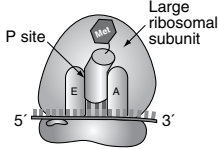
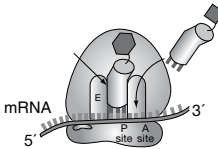
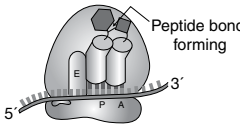
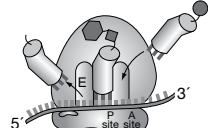
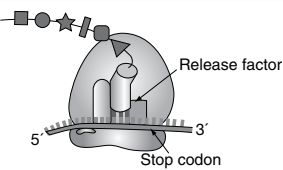
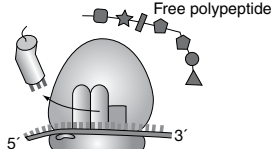
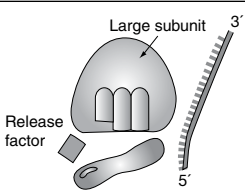


- 7.4.2.4** The basic structure and function of ribosomes are the same in bacteria, archaea and eukaryotes. However, eukaryotic ribosomes are slightly larger than prokaryotic ribosomes and have a slightly different composition. Eukaryotic ribosomes are 80S (Svedberg units which measure size and density), while prokaryotic ribosomes are 70S. The ribosomes in chloroplasts and mitochondria are 70S, which is used as an indicator of their evolutionary origin.
- 7.4.3.1** The main steps in translation are initiation, elongation, translocation and termination.
- 7.4.4.1** Translation occurs in a 5' → 3' direction.
- 7.4.4.2** The start codon is near the 5' end.
- 7.4.5.1**



- 7.4.6.1** A polysome or polyribosome is a cluster of ribosomes, bound to one mRNA.
- 7.4.6.2** The start codon on mRNA is AUG. This means the first tRNA has the anticodon UAC and the first amino acid is methionine.
- 7.6.6.3** A stop codon, e.g. UAG, UAA or UGA signals cessation of protein synthesis. There are no tRNA with anticodons complementary to a stop codon on mRNA.

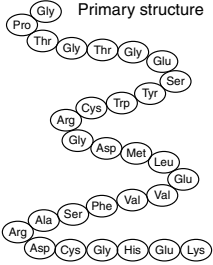
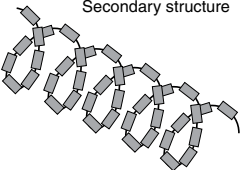
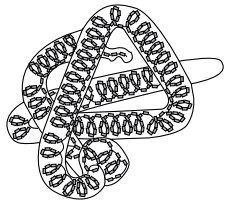
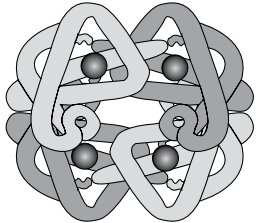
7.4.6.4

Stages of translation	
Diagram of stage	Description of stage
	Initiation: mRNA binds to the small ribosomal subunit at the mRNA binding site and the first tRNA with the anticodon UAC. The small subunit scans down the mRNA until it reaches the start codon AUG on the mRNA. When it reaches the start codon, translation begins.
	Final step in initiation: The large subunit attaches with the help of initiation factors. The first tRNA is at the P site of the ribosome.
	Elongation: A tRNA with the anticodon for the next codon on the mRNA pairs at the A site.
	A peptide bond forms between the new amino acid in the A site and the beginning of the forming polypeptide.
	The ribosome and mRNA move relative to each other so that the ribosome moves 5' → 3' along the mRNA. The tRNA at the E site is released and the next tRNA moves into the A position.
	Termination: When a stop codon, e.g. UAG, UAA or UGA reaches the A site, there is no corresponding tRNA with an amino acid and the code signals the halt of translation. A release factor binds to the stop codon at the A site.
	The release factor causes the release of the polypeptide from the tRNA at the P site and the polypeptide can move away from the ribosome. The last tRNA is released.
	The components dissociate and translation is complete.

7.4.7.1

Free ribosomes synthesise proteins for use within the cell, while bound ribosomes, e.g. on rough ER synthesise proteins for secretion, e.g. via Golgi body, or for lysosomes. The proteins synthesised by bound ribosomes are packaged into vesicles.

7.5.1.1

Diagram of protein	Description	Significance
Primary structure 	Primary structure is a linear sequence of amino acids. The amino acids are linked together with peptide bonds. There are 20 different amino acids which can link together in a vast number of combinations. The arrangement of polar R groups and non-polar R groups of the amino acids causes attraction and repulsion points.	The sequence of amino acids is extremely important as it influences higher levels of organisation in the protein and its biological function.
Secondary structure 	Secondary structures are coils or folds caused by hydrogen bonds between repeating CO and NH groups. Secondary structures include the helix and β pleated sheet.	Pleated sheets make up the basis of many globular proteins and fibrous proteins, e.g. keratin a fibrous protein consists mainly of α -helices while silk protein is also a fibrous protein but is mainly β -sheet form.
Tertiary structure 	Tertiary structure is formed by folding of the secondary structure into a complex and compacted shape. The shape is determined by interactions between the R groups of the amino acids, hydrophobic interactions, hydrophilic interactions and hydrogen bonding. Disulfide bridges are strong covalent links, e.g. between neighbouring cysteine amino acids and can stabilise the structure.	The folding of tertiary structures can provide structural strength, e.g. microtubules are globular proteins, or can produce an 'active site', e.g. enzymes are globular proteins.
Quaternary structure 	Quaternary structure involves the interaction between several polypeptide chains. The individual subunits are held together by hydrogen bonds rather than covalent linkages, though disulfide bonds occur. Conjugated proteins contain non-protein material and the non-protein part is called the prosthetic group.	Many important proteins use quaternary structure to carry out a large variety of biological functions, e.g. collagen fibres and haemoglobin. Conjugated proteins include chlorophyll and many enzymes in the electron transport chain.

7.5.2.1

Characteristic	Fibrous protein	Globular protein
Shape	Long.	Globe-like, tightly compact and folded into complex shapes.
Polypeptide chains	In long fibres or sheets using secondary structure.	Folded into a spherical shape induced by tertiary structure.
Properties	Water insoluble. Physically strong, can be supple or stretch easily.	Water soluble where they form colloidal solution.
Examples and function	Structural, e.g. collagen in cartilage, bones, tendons, connective tissue. Keratin in hair, fingernails. Elastins, e.g. myosin and actin in muscles.	Enzymes – catalyse reactions, e.g. esterases. Messengers, e.g. hormones such as insulin. Transporters, e.g. haemoglobin carrying oxygen. Defence, e.g. immunoglobulins and antibodies. Some structural functions, e.g. part of cell membrane which is structural as well as assisting in transporting ions in and out of the cell.

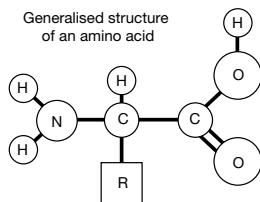
7.5.3.1

All amino acids have an amine group (NH_2), a carboxyl group (COOH) and a side chain (R). The different chemical properties of different amino acids, e.g. polar (hydrophile) or non-polar (hydrophobe) depend on the properties of R.

7.5.3.2

The distribution of hydrophilic and hydrophobic amino acids in a protein determines the tertiary structure which in turn determines the quaternary structure of the protein. This is highly important as it determines the properties of the protein and thus its biological function. Soluble proteins will need to contain a large number of polar amino acids such as threonine while integral membrane proteins need to be in the bilipid layer and thus need to have an arrangement of polar and non-polar amino acids to anchor them in the membrane. Thus the polar/non-polar property of an amino acid has a significant effect on the properties of a protein.

7.5.3.3



7.5.3.4 The arrangement of the non-polar amino acids and polar amino acids causes insulin to form a ball with the non-polar amino acids clumped together inside and the polar amino acids outside. This is typical of globular proteins. The presence of the disulfide bonds folds the insulin into its correct conformation to become active. Thus the arrangement of the amino acids and bonds give insulin its shape.

7.5.4.1

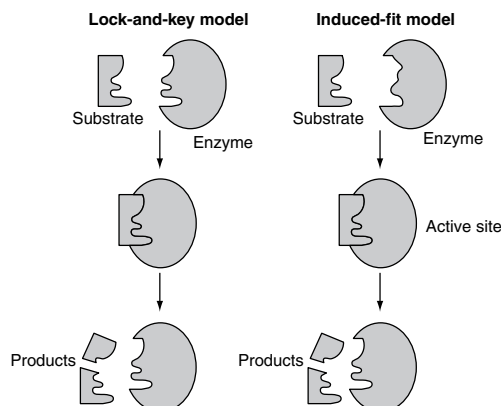
Function	Description of function	Example
Enzyme	Enzymes catalyse organic reactions and control the rate of metabolism. Enzymes are globular proteins and have an active site formed by the folding of the polypeptide chain into a specific shape.	Catalase is an enzyme that controls the breakdown of hydrogen peroxide into water and oxygen. Most cells form hydrogen peroxide (H_2O_2) as a waste product of aerobic respiration.
Hormone	Hormones act on specific target cells to change their functioning. Hormones are globular proteins.	Insulin is a hormone that is produced in the pancreas in the beta cells of the islets of Langerhans. When blood sugar exceeds a certain level insulin is released and it causes the liver to take up glucose and store it as glycogen.
Structure	Fibrous proteins form long fibres or sheets. Crosslinks can form between the fibres providing properties to make the fibre tough, supple or elastic.	Collagen fibres form a rope with three helical polypeptides wound around each other. Strands are held together by hydrogen bonds. Collagen accounts for around half the total protein in the human body.
Transport	Proteins are involved in transporting molecules across cell membranes and in the bloodstream.	Haemoglobin is a conjugated globular protein with four subunits (haem). Each haem has an iron atom that can bind with oxygen. Haemoglobin transports oxygen from oxygen-rich areas, e.g. capillaries around an alveolus to other areas where the oxygen is unloaded.

7.6.1.1 Metabolic pathways are a series of chemical reactions. The reactions can be catabolic and breakdown large molecules into smaller molecules, or anabolic and synthesise large molecules from smaller molecules.

7.6.1.2 Enzymes catalyse the reaction and control the rate of a reaction within a metabolic pathway. The enzyme is not consumed in the reaction.

7.6.2.1 The active site is a restricted region of the enzyme which binds to the substrate. It is formed by a few of the amino acids present in the protein and determines the specificity of the enzyme.

7.6.2.2



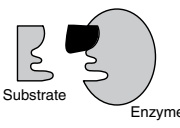
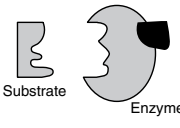
7.6.2.3 The development of a scientific theory involves observation, hypothesis, data collection and rejection or acceptance of the hypothesis. Our understanding of how enzymes act on their substrates began when Emil Fischer introduced the lock-and-key model in 1890. As further data was collected, the model needed to be modified and in 1958 Daniel Koshland suggested the induced-fit model where the binding of the enzyme to the substrate involved a change in shape of the enzyme to fit the substrate at the active site. The development of the induced-fit model shows how scientific theories are developed from observation, data collection and then modification of the theory when further data collection provides greater detail about the process.

7.6.3.1 The graph shows exothermic reactions – energy is released with the energy levels of the reactants higher than the energy level of the products. The energy required for the reaction to proceed without an enzyme is higher than with an enzyme present. Enzymes lower the activation energy needed for a given reaction.

7.6.4.1 Competitive inhibition is a type of enzyme inhibition where an inhibitor binds to the enzyme with weak bonds and prevents the binding of the substrate to the enzyme.

7.6.4.2 Non-competitive inhibition is a type of enzyme inhibition where the inhibitor reduces the ability of the enzyme to bind with the substrate without competing with the enzyme for the active site.

7.6.4.3

Diagram	Type of inhibition	How inhibition works	Example
	Competitive inhibition	The competitive inhibitor binds with the enzyme and competes with the substrate for the active site.	Methanol poisoning is caused by the oxidation in the body of methanol by formaldehyde oxidase to formaldehyde and formic acid which attack the optic nerve and cause blindness. Treatment for methanol poisoning involves giving the patient ethanol. The ethanol is a competitive inhibitor for formaldehyde oxidase and is oxidised in preference to methanol and thus prevents the build-up of the toxic by-products.
	Non-competitive inhibition	The non-competitive inhibitor binds to the enzyme away from the active site and alters the enzyme so that the enzyme can no longer bind with the substrate.	Heavy metal poisoning, e.g. silver (Ag^+) is caused when the silver binds with the enzyme away from the active site and this causes a change in the shape of the active site so that the enzyme can no longer function properly.

7.6.5.1 An allosteric regulated enzyme is an enzyme, usually made from two or more polypeptide chains, that can be regulated by a molecule that binds to one site in the enzyme and affects the functioning of the enzyme at a different site.

7.6.5.2 An allosteric site or the regulatory site is the section of the enzyme where the activating or inhibitory regulatory molecules bind to the enzyme.

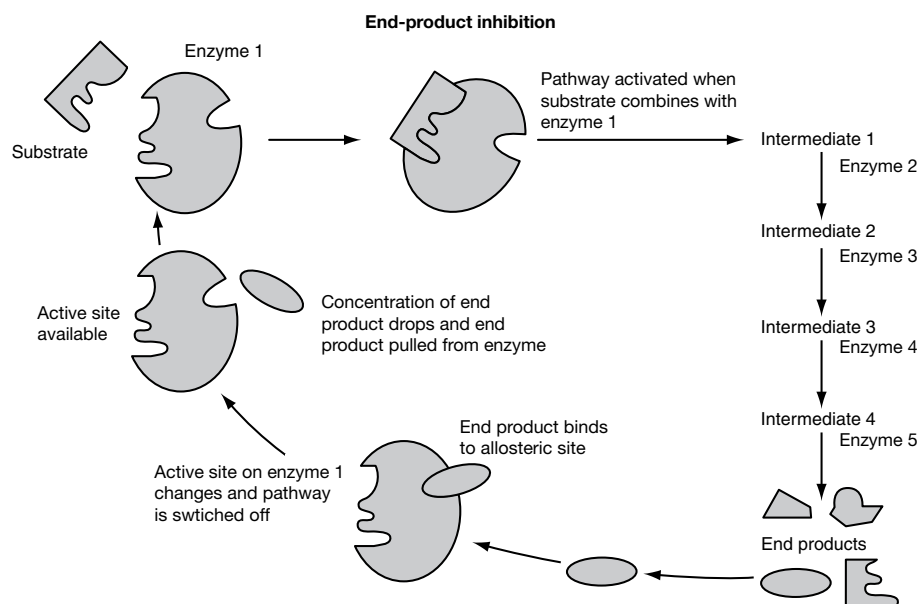
7.5.6.3 Allosteric activators and allosteric inhibitors are both regulatory molecules that can affect the functioning of an enzyme. Allosteric activators can speed up the reaction while allosteric inhibitors slow down the reaction.

7.6.5.4 The diagram shows how there is an active form of the enzyme and an inactive form of the enzyme. When the inhibitor joins with the enzyme at the allosteric site, the enzyme is stabilised into its inactive form. When the activator joins with the enzyme at the allosteric site, the enzyme is stabilised into its active form.

7.6.5.5 Cooperativity occurs when an enzyme with two or more subunits has one active site triggered into the active shape by a substrate molecule and this causes all the other active sites to be triggered into the induced-fit form.

7.6.5.6 End-product inhibition is a feedback mechanism in a multistep pathway where the end product binds to an enzyme that is early in the chain of reactions. This inhibits the series of reactions and prevents the production of more end product.

7.6.5.7





- 7.6.5.8** In mixed inhibition the inhibitor can bind to the enzyme as well as the enzyme's substrate. This usually occurs due to the allosteric effect as the inhibitor binds to a different site on the enzyme.
- 7.6.5.9** Many drugs resemble the substrate for specific reactions as a way to block that particular reaction. The pathogen would be carrying out the reaction and releasing a particular enzyme. The drug will act as an inhibitor and stop the metabolic pathway in the pathogen, e.g. drugs used to treat HIV act as protease inhibitors and compete for the active site on the enzyme with the substrate.